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Restriction Map of the RSV G Gene

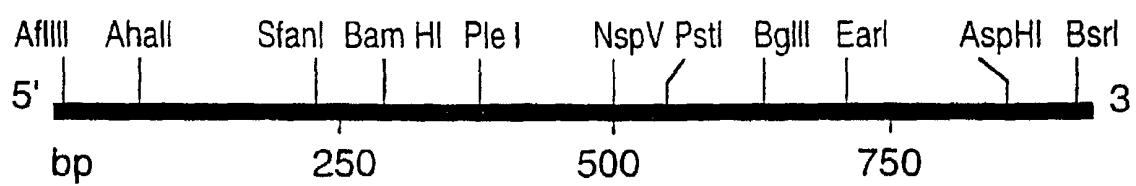


FIG.1

FIG.2A



10	19	28	37	46	55
TGCCAAC ATG TCC AAA AAC AGC GAC CAA CGC ACC GCT AAG ACA CTA GAA AAG ACC					
Met Ser Lys Asn Lys Asp Gln Arg Thr Ala Lys Thr Leu Glu Lys Thr					
64	73	82	91	100	109
TGG GAC ACT CTC AAT CAT TTA TTC ATA TCA TCG GGC TTA TAT AAG TTA AAT					
Trp Asp Thr Leu Asn His Leu Leu Phe Ile Ser Ser Gly Leu Tyr Lys Leu Asn					
118	127	136	145	154	163
CTT AAA TCT GTA GCA CAA ATC ACA TTA TCC ATT CTG GCA ATG ATA ATC TCA ACT					
Leu Lys Ser Val Ala Gln Ile Thr Leu Ser Ile Leu Ala Met Ile Ile Ser Thr					
172	181	190	199	208	217
TCA CTT ATA ATT ACA GCC ATC ATC TTA TTC ATA GCC TCG GCA AAC CAC AAA GTC ACA					
Ser Leu Ile Ile Thr Ala Ile Ile Phe Ile Ala Ser Ala Asn His Lys Val Thr					
226	235	244	253	262	271
CTA ACA ACT GCA ATC ATA CAA GAT GCA ACA AGC CAG ATC AAG AAC ACA ACC CCA					
Leu Thr Thr Ala Ile Gln Asp Ala Thr Ser Gln Ile Lys Asn Thr Thr Pro					
280	289	298	307	316	325
ACA TAC CTC ACT CAG GAT CCT CAG CTT GGA ATC AGC TTC TCC AAT CTG TCT GAA					
Thr Tyr Leu Thr Gln Asp Pro Gln Leu Gly Ile Ser Phe Ser Asn Leu Ser Glu					



FIG. 2B

FIG.2C

658	667	676	685	694	703
CTC AAA CCT CAA ACC ACT AAA CCA AAG GAA GTC CCC ACC ACC AAG CCC ACA GAA					
Leu Lys Pro Gln Thr Thr Lys Pro Lys Glu Val Pro Thr Thr Lys Pro Thr Glu					
712	721	730	739	748	757
GAG CCA ACC ATC AAC ACC ACC AAA ACA AAC ATC ACA ACT ACA CTG CTC ACC AAC					
Glu Pro Thr Ile Asn Thr Thr Lys Thr Asn Ile Thr Thr Thr Leu Leu Leu Thr Asn					
766	775	784	793	802	811
AAC ACC ACA GGA AAT CCA AAA CTC ACA AGT CAA ATG GAA ACC TTC CAC TCA ACC					
Asn Thr Thr Gly Asn Pro Lys Leu Thr Ser Gln Met Glu Thr Phe His Ser Thr					
820	829	838	847	856	865
TCC TCC GAA GGC AAT CTA AGC CCT TCT CAA GTC TCC ACA ACA TCC GAG CAC CCA					
Ser Ser Glu Gly Asn Leu Ser Pro Ser Gln Val Ser Thr Thr Ser Glu His Pro					
874	883	892	901	914	
TCA CAA CCC TCA TCT CCA CCC AAC ACA ACA CGC CAG TAGTTATTAA AAAAAGAA					
Ser Gln Pro Ser Ser Pro Pro Asn Thr Arg Gln .					

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FIG.3A

CAC AAA GTC ACA CTA ACA ACT GCA ATC ATA CAA GAT GCA ACA AGC CGC ATC AAG	54
His Lys Val Thr Leu Thr Thr Ala Ile Ile Gln Asp Ala Thr Ser Gln Ile Lys	18
AAC ACA ACC CCA ACA TAC CTC ACT CAG GAT CCT CAG CTT CGA ATC AGC TTC TCC	108
Asn Thr Thr Pro Thr Tyr Leu Thr Gln Asp Pro Gln Leu Gly Ile Ser Phe Ser	36
AAT CTG TCT GAA ATT ACA TCA CAA ACC ACC ATA CTA GCT TCA ACA ACA CCA	162
Asn Leu Ser Glu Ile Thr Ser Gln Thr Thr Ile Leu Ala Ser Thr Thr Pro	54
GGA GTC AAC CTG CAA CCC ACA ACA GTC AAG ACT AAA AAC ACA ACA ACA	216
Gly Val Lys Ser Asn Leu Gln Pro Thr Thr Val Lys Thr Lys Asn Thr Thr Thr	72 5 / 19
ACC CAA ACA CAA CCC AGC AAG CCC ACT ACA AAA CAA CCA CGC CAA AAC AAA CCA CCA	270
Thr Gln Thr Gln Pro Ser Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro	90
AAC AAA CCC AAT AAT GAT TTT CAC TTC GAA GTG TTT AAC TTT GTT CCC TGC AGC	324
Asn Lys Pro Asn Asn Asp Phe His Phe Glu Val Pro Cys Ser Ser	108
ATA TGC AGC AAC AAT CCA ACC TGC TGG GCT ATC TGC AAA AGA ATA CCA AAC AAA	378
Ile Cys Ser Asn Asn Pro Thr Cys Thr Ala Ile Cys Lys Arg Ile Pro Asn Lys	126
AAA CCA GGA AAG AAA ACC ACC AAG CCT ACA AAA AAA CCA ACC TTC AAG ACA	432
Lys Pro GLY Lys Lys Thr Thr Lys Pro Thr Phe Lys Pro Thr Phe Lys Thr	144

FIG.3B

ACC AAA AAA GAT CTC AAA CCT CAA ACC ACT AAA CCA AAG GAA GTA CCC ACC ACC	486
Thr Lys Lys Asp Leu Lys Pro Glu Val Pro Thr Thr Thr	162
AAG CCC ACA GAA GAG CCA ACC AAC ATC ACC ACC AAA ACA AAC ATC ACA ACT ACA	540
Lys Pro Thr Glu Glu Pro Thr Ile Asn Thr Thr Lys Thr Asn Ile Thr Thr Thr	180
CTG CTC ACC AAC ACC ACA GGA AAT CCA AAA CTC ACA AGT CAA ATG GAA ACC	594
Leu Leu Thr Asn Asn Thr Thr Gly Asn Pro Lys Leu Thr Ser Glu Met Glu Thr	198
TTC CAC TCA ACC TCC TCC GAA CGC AAT CTA AGC CCT TCT CAA GTC TCC ACA ACA	648
Phe His Ser Thr Ser Ser Glu Gly Asn Leu Ser Pro Ser Glu Val Ser Thr Thr	216
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TCC GAG CAC CCA TCA CAA CCC TCA TCT CCA CCC AAC ACA ACA CGC CAG TAG	699
Ser Glu His Pro Ser Ser Gln Pro Pro Asn Thr Arg Gln	232
TTATTA AAAAAAAA	

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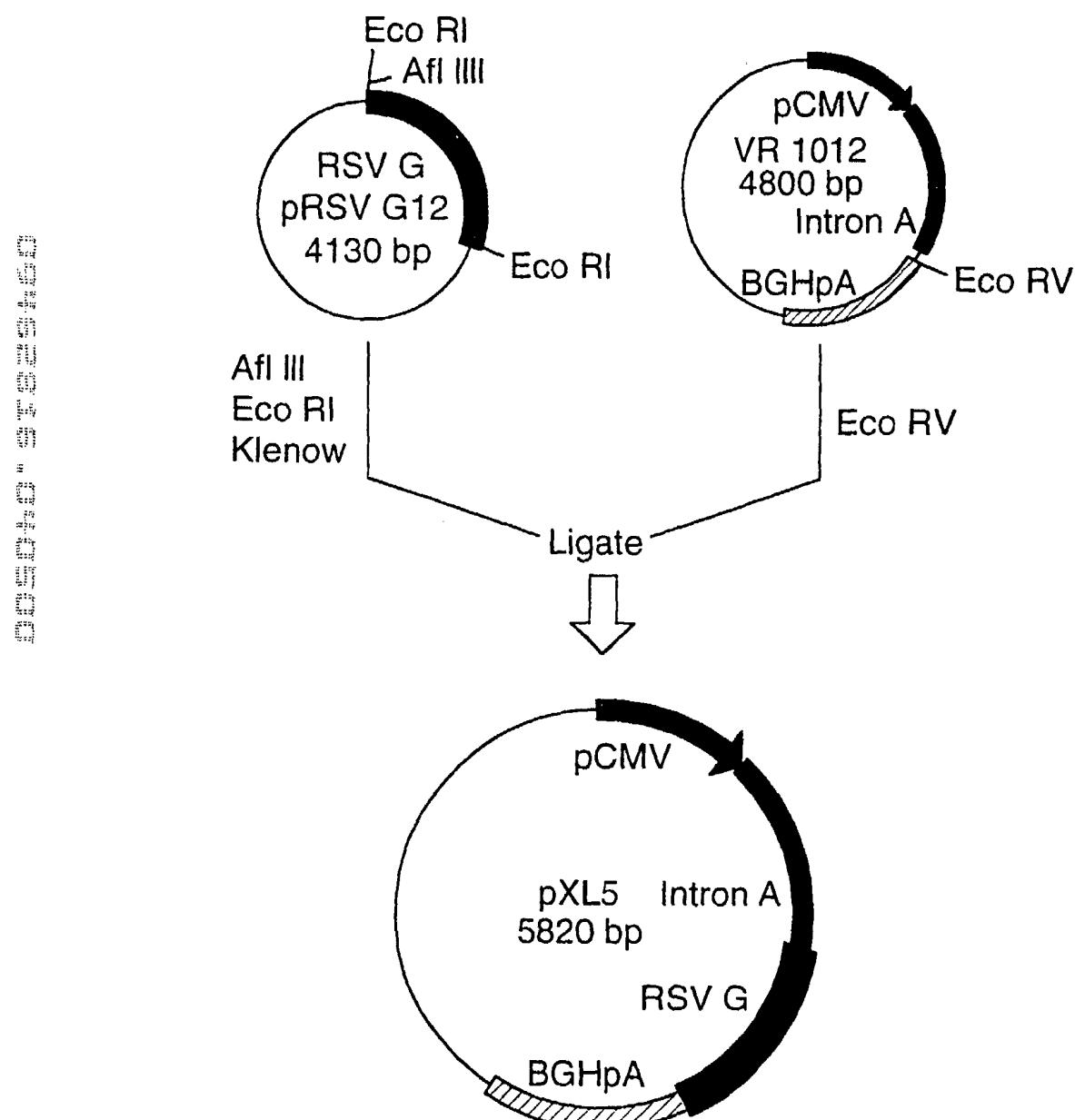


FIG. 4.

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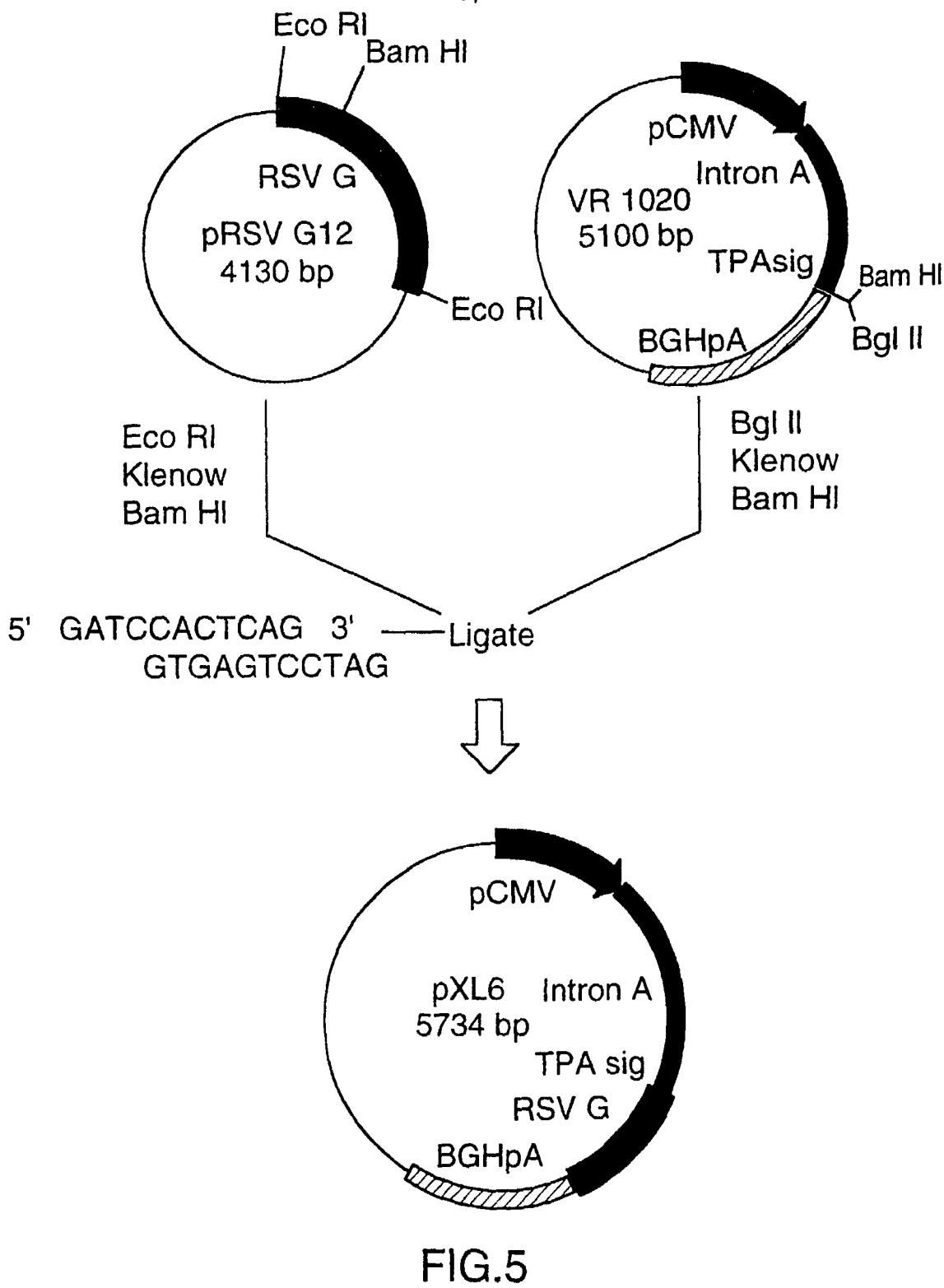


FIG. 6A

10	20	30	40	50	60	70
TGCCCCGTT	CGGTGATGAC	GTTGAAACC	TCTGACACAT	CCACCTCCCC	GAGACCGTCA	CAGCTTGTCT
80	90	100	110	120	130	140
GTAAGGGAT	CCCCGGCA	GACAAGCCG	TCAAGGGCG	TCACCCCGTC	TTCGGCGGTG	TGGGGCGCTGG
150	160	170	180	190	200	210
CTTAACATAG	CGGCCATCAGA	GCAGATTGTA	CTGAGACTGC	ACCATAATGGG	GTGTGAATA	CCGGCACAGAT
220	230	240	250	260	270	280
GCGTAAGGAG	AAAATACCGC	ATCAGATTGG	CTATTGCCA	TTCGATACGT	TGTATCCATA	TCATAATAATG
290	300	310	320	330	340	350
TACATTATA	TTCGCTCATG	TCCAACATTA	CCGCCATGTT	GACATTGATT	ATTGACTAGT	TATTAAATGT
360	370	380	390	400	410	420
AATCAATTAC	GGGTCAATTA	GGTCAATGCC	CATATAATGGA	GTTCGGCGTT	ACATAACITA	CCGGTAATAGC
430	440	450	460	470	480	490
CCGGCTTGCC	TGACCGCCA	ACCAACCCCG	CCCATTTGACG	TCAATAATGA	CGTATACGTC	CATAGTAACG
500	510	520	530	540	550	560
CCATTAGGA	CTTCCTATTG	AGTCATTG	GTGGAGTATT	TACGGTAAC	TCGGCACTTG	GCAGTACATC

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FIG. 6B

570	580	590	600	610	620	630
AAGTGTATCA	TATGCGAAGT	ACGCCCGCTTA	TTCGACGTCAA	TGAAACGGTAAA	TGGCCAGCCT	GGCATTTATGC
640	650	660	670	680	690	700
CCAGTACATG	ACCTTAATGGG	ACTTTTCCCTAC	TTCGGCAGTAC	ATCTAACGTAT	TAGTCATCGC	TATTACCATG
710	720	730	740	750	760	770
GTCATTCCTG	TTTCGCACTGA	CATCAATGGG	CGTCGATAGC	CGTTTGACTC	ACGGGGATT	CCAAGTCTCC
780	790	800	810	820	830	840
ACCCATTCA	CGTCATAATGGG	AGTTTGTTT	GGCACCAAAA	TCAACGGGAC	TTTCACAAAT	GTGCGTAACAA
850	860	870	880	890	900	910
CTCGGCCCA	TTGACCCAAA	TGGGGCTTAG	GGCTGTACGG	TGGCAGGTCT	ATATAAGGAG	AGCTTCGTTA
920	930	940	950	960	970	980
GTCACCGTC	AGATCGCTG	GACACCGCAT	CCACCGCTGT	TTCACCTCA	TAGAGACAC	CGGGCAACGAT
990	1000	1010	1020	1030	1040	1050
CCAGCCTCCG	CCCCCGGAA	CGCTGCATTG	GAACCGGAT	TCCCGCTGCC	AAGAGTGAAG	TAAGTACCGC
1060	1070	1080	1090	1100	1110	1120
CTATAGACTC	TATAGCCACA	CCCGCTTGGC	TCTTATACAT	GCTTATACAT	TTCGGCTTC	GGGCTTATAC

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PCT/CA98/00697

FIG.6C

1130 1140 1150 1160 1170 1180 1190
ACCCCGCTT CCTTATGCTA TAGGTGATGG TATAGCTTAG CCTATAAGTG TGGTTATTG ACCATTATTG
1200 1210 1220 1230 1240 1250 1260
ACCACTCCC TATTCGGAC GATACTTTC ATTACTAAC CATAACATGG CTCCTGGCA CAACTATCTC
1270 1280 1290 1300 1310 1320 1330
TATTGGCTAT ATGCCAATAC TCTGTCCTTC AGAGACTGAC ACGGACCTG TATTITACA GGATGGGTC
1340 1350 1360 1370 1380 1390 1400
CCATTATTAA TTACAAATT CAATATACA ACACGGCGT CCACCGGCC CCAGTTTTT ATTAAACATA
1410 1420 1430 1440 1450 1460 1470
GGCTGGGATC TOCACCGAA TCTGGGTAC GGTTGGGA CATGGCTCTT TCTGGTAG CGGGGAGCT
1480 1490 1500 1510 1520 1530 1540
TCCACATCG ACCCCTGGTC CCATGCCCTC ACCGGCTCAT CGTCCTCG CAGCTCTG CTCTAACAG
1550 1560 1570 1580 1590 1600 1610
TGGAAGCCAG ACTTAGGCAC AGCACAAATGC CCACACCAC CAGTGTGGCG CACAAAGCGC TGGCGTAGG
1620 1630 1640 1650 1660 1670 1680
GTATGGCTCT GAAAATGACC GTGGAGATIG CGCTCCACCG GCTCAOGCG ATGGAGACT TAACCCACCG
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FIG. 6D

1690	1700	1710	1720	1730	1740	1750
GCAGAAAGAAG	ATGCCACCGAG	CTCAGTTGTT	GTATTCTCAT	AACAGTACA	GGTAACCTCC	GTTCGGGTG
1760	1770	1780	1790	1800	1810	1820
TGTTAACGGT	GGACGGCAGT	GTAGTCAG	CAGTACTCGT	TCTTCGGCG	AGGCCACCA	GACATAATTAG
1830	1840	1850	1860	1870	1880	1890
CTGACAGACT	AACAGACTGT	TCCTTCCAT	GGGTCTTTC	TCCAGTCACC	GTCTCTGACA	CGTGATCA
1900	1910	1920	1930	1940	1950	1960
GATATGGGG	CCGCTCTAGA	CCAGGGCT	GGATOCAGAT	CTCTCTGCC	TTCCTAGTGC	CAGCCATCTG
1970	1980	1990	2000	2010	2020	2030
TGTTTCCCC	CTCCCCGTG	CTTTCCTGA	CCCTGAAAGG	TGCCACTCC	ACTGTCCTT	OCTAATAAA
2040	2050	2060	2070	2080	2090	2100
TGAGCAAATT	GCATGGCATT	GTCTGAGTAG	GTGTCATTCT	ATTCTCTGGG	GTCTCTGGG	GCAGGGACAGC
2110	2120	2130	2140	2150	2160	2170
AACGGGGAGG	ATTCCGAAGA	CAATAGCAGG	CAATCTGGG	ATGCCCTGG	CTCTATGGT	ACCCAGGT
2180	2190	2200	2210	2220	2230	2240
TCAAGAATTG	ACCCGGTTC	TCTTGGCCA	GAAGAGAGCA	GGCACATCCC	CTCTCTGTG	ACACACCCG

FIG. 6E

2250	2260	2270	2280	2290	2300	2310
TCCACCCCCC	TTCTCTTAG	TTCCAGCCCC	ACTCATAGGA	CACTCATAGC	TCAGGAGGCC	TCCGGCTTCA
2320	2330	2340	2350	2360	2370	2380
ATCCCACCGG	CTAAAGTACT	TCGACCGGTG	TCTCCCTCCC	TCATCACCCC	ACCAAACCAA	ACCTAGCCTC
2390	2400	2410	2420	2430	2440	2450
CAAGAGTGGG	AGGAATTAA	AGCAAGATAG	GCTTATAAAGT	GCAGAGGGAG	AGAAAATGCC	TCCAACATGT
2460	2470	2480	2490	2500	2510	2520 / 19
GAGGAAGTAA	TCAGAGAAAT	CATAGAATT	CTTCGGCTTC	CTCGCTCACT	GACTCGCTCC	GCTCGGGCTG
2530	2540	2550	2560	2570	2580	2590
TGGCTCTGGG	CGACCGGTAT	CACCTCACTC	AAAGCCGGTA	ATACCGTTAT	CCACAGAAC	ACCCGATAAC
2600	2610	2620	2630	2640	2650	2660
GGAGGAAACA	ACATGTTGAGC	AAAAGGCCAG	CAAAGGCCA	CGAACCGTAA	AAAGGCCGCG	TTGCTGGGT
2670	2680	2690	2700	2710	2720	2730
TTTTCATAG	GCTCCCCCCC	CTTGACGGAGC	ATCACAAAAA	TGGACCTCA	AGTCACAGGT	GGCGAAACCC
2740	2750	2760	2770	2780	2790	2800
GACAGGACTA	TAAGATACC	AGGGCTTCC	CCCTGGAGCC	TCCCTCTCTG	GCTCTCTGT	TCCGACCTG

FIG. 6F

2810	2820	2830	2840	2850	2860	2870
CCGCTTACCG	GATACTGTG	GGCCTTTCCTC	CCTTCGGAA	GGTGTGGCT	TTCATAGC	TCAAGCTGTGA
2880	2890	2900	2910	2920	2930	2940
GGTATCTAG	TTCGGTGTAG	GTCGTTGCT	CCAAGCTGG	CTGTTGCAC	GAACCCCCG	TTCAGCCCCA
2950	2960	2970	2980	2990	3000	3010
CCGCTGGCC	TTATCCGTA	ACTATCGTCT	TGACTCCAAC	CCCTTAAGAC	ACGACTTATC	GCCACTUGCA
3020	3030	3040	3050	3060	3070	3080
GGACCCACTG	GTAAACAGGAT	TAGCACAGGG	AGGTAATGTA	GGCGGCTAC	AGAGTTCTTG	AAGTGGTGGC
3090	3100	3110	3120	3130	3140	3150
CTAACTACGG	CTACACTAGA	AGAACAGTAT	TTCGTATCTG	CCCTCTGCTG	AAGCCAGTTA	CTTTCGAAA
3160	3170	3180	3190	3200	3210	3220
AAGAGTTGGT	ACCTCTGAT	CCGCCAAACA	AACCACCGT	CGTAGGGTG	GTTTTTGT	TTCGAAGCAG
3230	3240	3250	3260	3270	3280	3290
CAGATTACGC	GCACAAAAAA	AGGATCTCAA	GAAGATCTT	TGATCTTTTC	TACGGGGTCT	GACGGCTCAGT
3300	3310	3320	3330	3340	3350	3360
GGAACCGAAAA	CTGACGTTAA	GGCAATTGCG	TCATGAGATT	ATCAAAAGG	ATCTTCACCT	AGATCTTTT

FIG. 6G

3370 3380 3390 3400 3410 3420 3430
 AAATTAAAAA TGAAGTTTA AATCATACTA AAGTATATAT GAGTAAACTT CGTCTCACAG TTACCAATGC

 3440 3450 3460 3470 3480 3490 3500
 TTATCAGTC AGGCACCTAT CTCAGCGATC TGCTATATTIC GTTCATCCAT AGTTCCTCA CTGGGGGGG

 3510 3520 3530 3540 3550 3560 3570
 GGGGGGCTG AGGTCTGCCT CGTCAAGCAAG GTGTTGGTA CTCATACCG GCCTGAATUG CCCCATCATC

 3580 3590 3600 3610 3620 3630 3640 15/19
 CAGCCAGAA GTCAAGGGAGC CACCGTTAT GAGAGCTTG TGTAGGTGG ACCAGTTGGT GATTITGAAAC

 3650 3660 3670 3680 3690 3700 3710
 TTTTGCTTG CCACCGAACG GTCTGGGTG TCGGGAACAT GCGTGTATCG ATCCCTCAC ACAGCAAAAG

 3720 3730 3740 3750 3760 3770 3780
 TTGATTATT TCAACAAAGC CCCCGTCCCG TCAAGTCAGC GTAATGCTT GCGAGGTTA CAACCAATTAA

 3790 3800 3810 3820 3830 3840 3850
 ACCCAATTGTC ATTACAAAAA CTCATCGAAC ATCAAAATGAA ACTGCAATT ATTCAATTCA CGTATTCAAA

 3860 3870 3880 3890 3900 3910 3920
 TACCATATT TIGAAAAGC CGTTTCIGTA ATGAAAGGAGA AAVACTCACCG AGGCAGTTCC ATAGGATGCC

FIG. 6H

3930	3940	3950	3960	3970	3980	3990
AATATCCTCG	TATCCGTCGT	CGATTCCGAC	TGICCAACA	TCAATACAAC	CTATTAATT	CCCCTCGCA
4000	4010	4020	4030	4040	4050	4060
AAAATAAGT	TATCAAGTCA	AAATCACCA	TGAGTCACCA	CTGAATCCGG	TGAGAATGGC	AAAAGCTTAT
4070	4080	4090	4100	4110	4120	4130
GCATTCTTT	CCAGACTTGT	TCAACAGGCC	ACCCATTAG	CTCGTCATCA	AAATCACTCG	CATCAAACCAA
4140	4150	4160	4170	4180	4190	4200
ACCGTTATTC	ATTGTCATT	GGCCCTGAGC	GAGAGAAAT	ACCGGATGCG	TGTAAAAGG	ACAATTACAA
4210	4220	4230	4240	4250	4260	4270
ACAGGAATTG	AATCCAACCG	GGCCAGGANC	ACTGCCAGCG	CATCAACAAT	ATTTCACCT	GAATCAGGAT
4280	4290	4300	4310	4320	4330	4340
ATTCTCTAA	TACCTGGAAT	GCTGTTTTC	CGGGGATGCG	AGTGGTGAGT	AACCATGCAT	CATCAGGAGT
4350	4360	4370	4380	4390	4400	4410
ACGGATAAAA	TGGCTTGATGG	TGGAAAGAGG	CATAAAATTCC	GTCAGCCAGT	TGAGTCGAC	CATCTCATCT
4420	4430	4440	4450	4460	4470	4480
GIAACATCAT	TGGCAACGGCT	ACCTTGGCA	TGTTTCAGAA	ACAACTCTGG	GGCATGGGC	TTCCCATACA

FIG. 6I

4490	4500	4510	4520	4530	4540	4550
ATCGATAGAT	TGTCGCCACT	GATTGCCGA	CATTATCGG	AGCCCAATTAA	TACCCATATA	ATTCAGGATC
4560	4570	4580	4590	4600	4610	4620
CATGTGGAA	TTAACATCGG	GCCTCGAGCA	AGACCGTTCC	CGTTGAATAT	GGCTCATAAC	GTTCCTTGTAA
4630	4640	4650	4660	4670	4680	4690
TTACTGTTA	TGTAGGCGAA	CAGTTTTATT	GTTCATGATG	ATATATTTT	ATCTCTGCCA	ATGTAACATC
4700	4710	4720	4730	4740	4750	4760
AGAGATTTG	AGACACAACG	TGGCTTCCC	CCCCCCCCCA	TATTTGAAGC	ATTATATAGG	GTATATGCT
4770	4780	4790	4800	4810	4820	4830
CATGAGCGGA	TACATATTG	AATGTATTTA	GAATAATAAA	CAAATAACGG	TTCAGGCCAC	ATTTCGCCGA
4840	4850	4860	4870	4880	4890	4900
AAAGTGCCAC	CTGACGCTTA	AGAAACCATT	ATTATCATGA	CATTAACTTA	TAAAAATAGG	CGTATCAGGA
4910						

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FIG.7

10 20 30 40 50 60 70
CTCCAGTCAC CGTGTGAC CACAGCTCAG ATCCATACAGG AGTCCAGGGC TGGAGAGAAA ACCCTCTGGGA

80 90 100 110 120 130 140
CGAAAGGCAA CGGAGCAAGCC GTGAAATTAA GGGACCCCTGT GAAGCCAATCA TGGATGCCAT GAAGAGAGGG

150 160 170 180
CTCTCTCTCTG TCCCTCTCTCT GTGTGGAGCA GTCTCTGTT CGCCCGAGC

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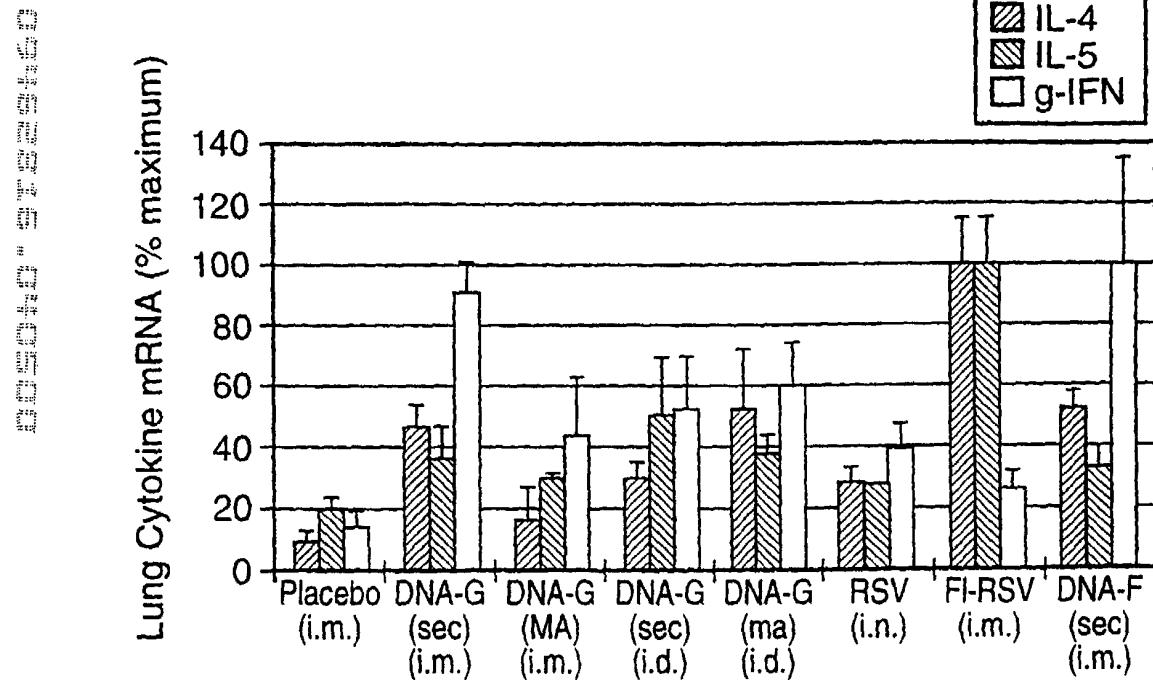


FIG.8